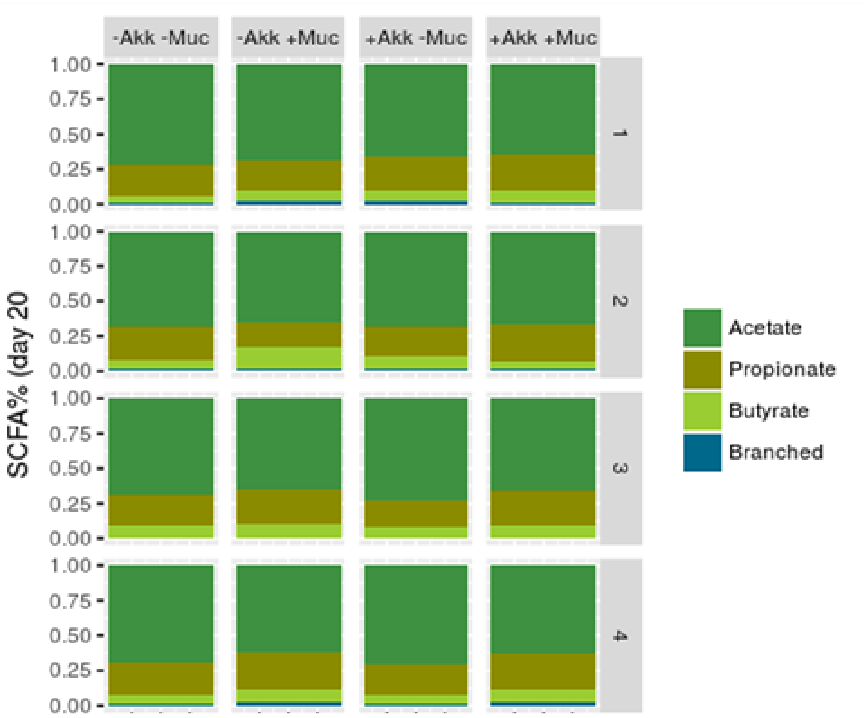
Supplementary information



Supplementary Figure 1: Proportions of acetate, propionate, butyrate and branched SCFA for the different donors and treatments at day 20.

Supplementary Table 1: RDP Seqmatch and NCBI BLAST results for the most abundant and relevant species in the microbial communities, as determined by amplicon sequencing. The similarity score (Sab) as calculated by RDP, and the NCBI BLAST output for the best hit and the next best hit(s) are shown.

		RDP	**NCBI BLAST**		
		Sab	**Query coverage (%)**	**E-score**	**Identity (%)**
OTU1	*Escherichia/Shigella fergusonii*	1	100	0	100
	Escherichia/Shigella flexneri	1	100	0	100
	Shigella sonnei	1	100	0	100
OTU2	*Clostridium bolteae*	1	100	0	100

	Clostridium clostridioforme	0,977	100	0	100
	Clostridium citroniae	0,964	100	0	99
OTU3	*Bacteroides ovatus*	0,961	100	0	99
	Bacteroides xylanisolvens	0,891	100	0	98
OTU4	*Fusobacterium varium*	0,995	100	0	100
	Fusobacterium ulcerans	0,928	100	0	99
OTU5	*Bacteroides uniformis*	1	100	0	100
	Bacteroides rodentium	0,906	100	0	97
OTU6	*Bacteroides dorei*	1	100	0	100
	Bacteroides vulgatus	0,954	100	0	99
OTU7	*Bilophila wadsworthia*	0,973			
	Desulfovibrio simplex	0,701	100	9E-173	92
OTU8	*Kluyvera cryocrescens*	0,983	100	0	99
	Enterobacter aerogenes	0,947	100	0	99
OTU9	*Akkermansia muciniphila*	1	100	0	100
	Verrucomicrobium spinosum	0,567	99	3E-107	84
OTU10	*Phascolarctobacterium succinatutens*	0,985	100	0	99
	Phascolarctobacterium faecium	0,723	100	0	94
OTU11	*Bacteroides thetaiotaomicron*	1	100	0	100
	Bacteroides faecichinchillae	0,947	100	0	99
OTU12	*Fusobacterium nucleatum*	0,982	100	0	99
	Fusobacterium simiae	0,946	100	0	99
OTU13	*Cloacibacillus porcorum*	0,929	100	0	99
	Cloacibacillus evryensis	0,837	100	0	96
OTU14	*Alistipes onderdonkii*	1	100	0	100
	Alistipes shahii	0,882	100	0	97

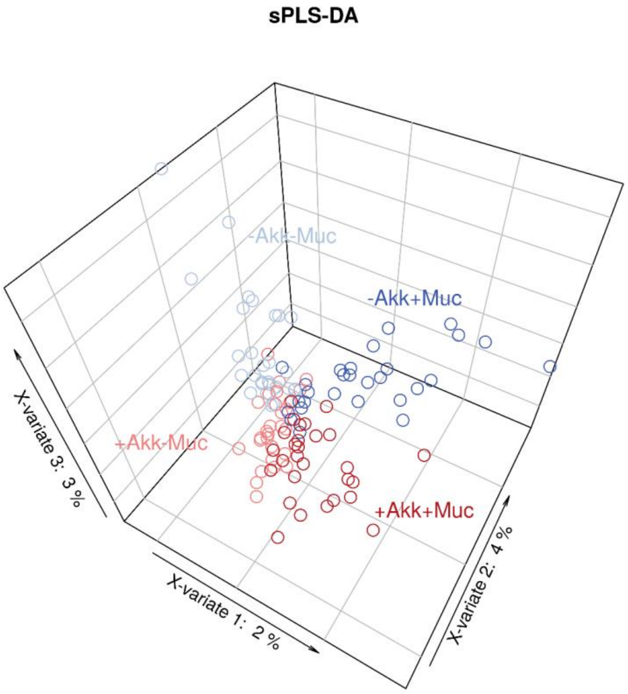
OTU15	*Bacteroides xylanisolvens*	1	100	0	100
	Bacteroides acidifaciens	0,959	100	0	99
OTU16	*Clostridium aldenense*	0,964	100	0	99
	Clostridium saccharolyticum	0,869	100	0	98
OTU17	*Veillonella tobetsuensis*	0,978	100	0	99
	Veillonella rogosae	0,971	100	0	99
OTU18	*Veillonella atypica*	0,956	100	0	99
	Veillonella dispar	0,932	100	0	98
OTU19	*Blautia coccoides*	1	100	0	100
	Blautia schinkii	0,985	100	0	98
OTU20	*Pseudomonas aeruginosa*	1	100	0	100
	Pseudomonas otitidis	959	100	0	99
OTU21	*Parasutterella excrementihominis*	1	100	0	100
	Parasutterella secunda	0,603	100	4E-166	91
OTU22	*Parabacteroides distasonis*	0,956	100	0	99
	Parabacteroides gordonii	0,664	100	4E-171	92
OTU23	*Citrobacter freundii*	1	100	0	100
	Raoultella terrigena	0,964	100	0	99
OTU24	*Bifidobacterium adolescentis*	1	100	0	100
	Bifidobacterium faecale	1	100	0	100
OTU25	*Bacteroides cellulosilyticus*	0,951	100	0	99
	Bacteroides intestinalis	0,92	100	0	99
OTU26	*Clostridium hathewayi*	1	100	0	100
	Clostridium xylanolyticum	0,879	100	0	97
OTU27	*Dialister invisus*	1	100	0	100
	Dialister propionicifaciens	0,839	100	0	95

OTU28	*Insolitispirillum peregrinum*	0,525	99	2E-127	87
	Novispirillum itersonii	0,525	99	9E-128	87
OTU29	*Enterobacter asburiae*	1	100	0	100
	Enterobacter xiangfangensis	1	100	0	100
OTU30	*Bacteroides acidifaciens*	0,889	100	0	96
	Bacteroides thetaiotaomicron	0,843	100	0	95
OTU32	*Clostridium hylemonae*	0,896	100	0	98
	Ruminococcus gnavus	0,83	100	0	96
OTU34	*Roseburia faecis*	0,949	100	0	99
	Eubacterium rectale	0,949	100	0	100
OTU37	*Clostridium xylanolyticum*	0,849	100	0	97
	Clostridium saccharolyticum	0,849	100	0	97
OTU41	*Enterobacter kobei*	0,983	100	0	99
	Enterobacter cloacae	0,966	100	0	99
OTU42	*Clostridium scindens*	1	100	0	100
	Clostridium hylemonae	0,843	100	0	96
OTU43	*Terrisporobacter glycolicus*	0,956	100	0	99
	Terrisporobacter mayombei	0,951	100	0	99
OTU44	*Selenomonas infelix*	0,983	100	0	99
	Selenomonas noxia	0,896	100	0	97
OTU45	*Blautia faecis*	1	100	0	100
	Blautia glucerasea	0,926	100	0	99
OTU46	*Selenomonas infelix*	0,923	100	0	98
	Selenomonas noxia	0,897	100	0	97
OTU48	*Ruminococcus torques*	0,98	100	0	99
	Ruminococcus faecis	0,89	100	0	98

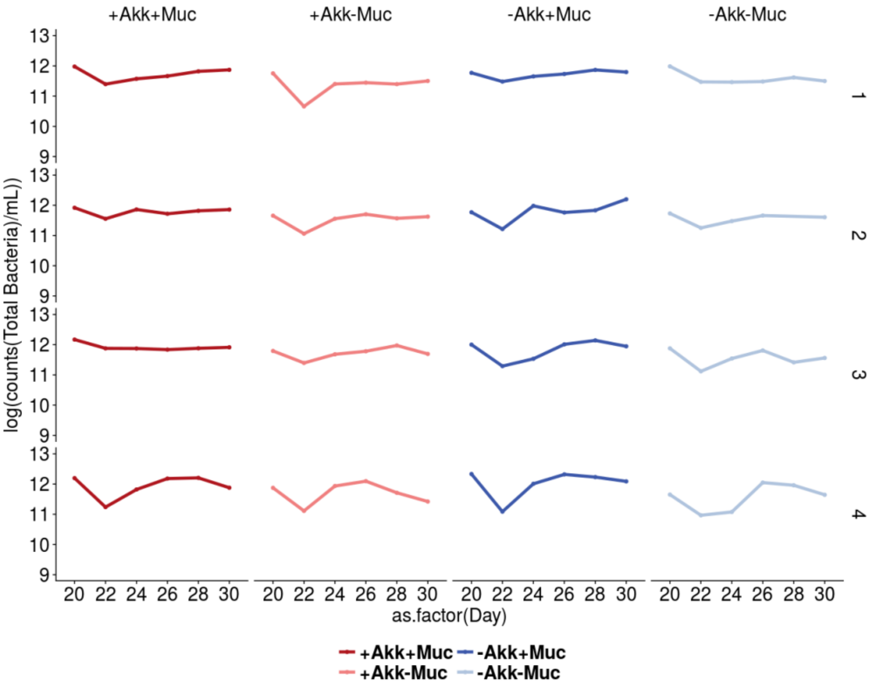
OTU53	*Stenotrophomonas maltophilia*	0,978	100	0	98
	Stenotrophomonas pavanii	0,894	100	0	98
OTU60	*Murimonas intestini*	1	100	0	100
	Ruminococcus lactaris	0,877	100	0	97
OTU65	*Ruminococcus torques*	0,87	100	0	96
	Ruminococcus lactaris	0,826	100	0	97
OTU78	*Clostridium colinum*	0,83	100	0	96
	Eubacterium ventriosum	0,638	100	2E-149	90
OTU100	*Lactonifactor longoviformis*	0,811	100	0	96
	Roseburia intestinalis	0,749	100	4E-176	94
OTU119	*Anaerofilum pentosovorans*	0,861	100	0	97
	Anaerofilum agile	0,843	100	0	97
OTU130	*Clostridium lactatifermentans*	0,741	100	3E-167	93
	Clostridium propionicum	0,723	100	6E-179	95

Supplementary Table 2: Partial distance based redundancy analysis. The contribution of the different factors, and significance level, to the variation in species level community composition.

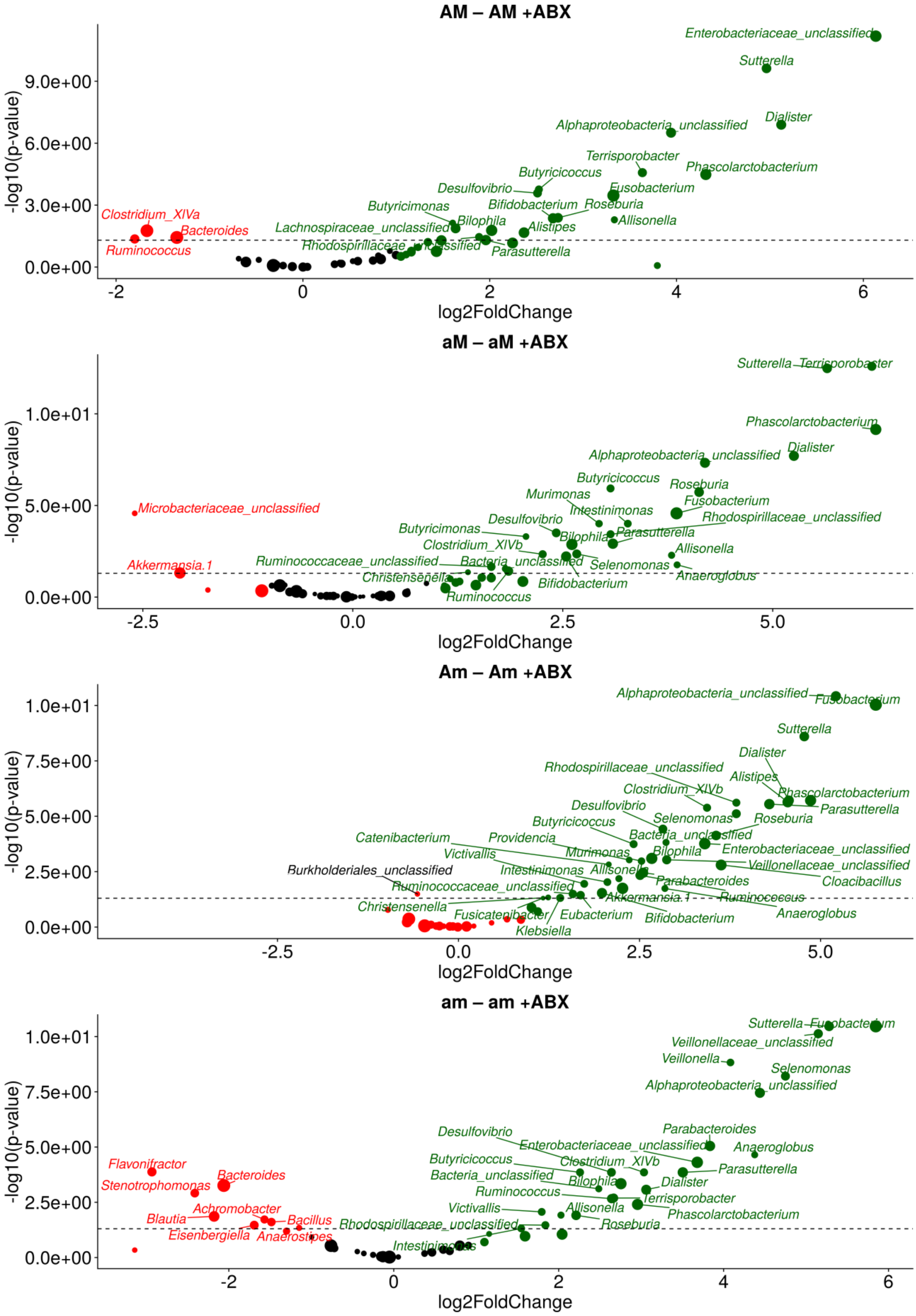
	% variance explained	**p-value**
Donor	14%	0.041
Treatment	20%	0.346
Mucin	8%	0.197
A. muciniphila	7%	0.278



Supplementary Figure 2: Optimal sPLS-DA model, as determined by fivefold cross-validation, retaining the species most predictive of the different treatments (+Akk+Muc; +Akk-Muc; -Akk+Muc; -Akk-Muc).

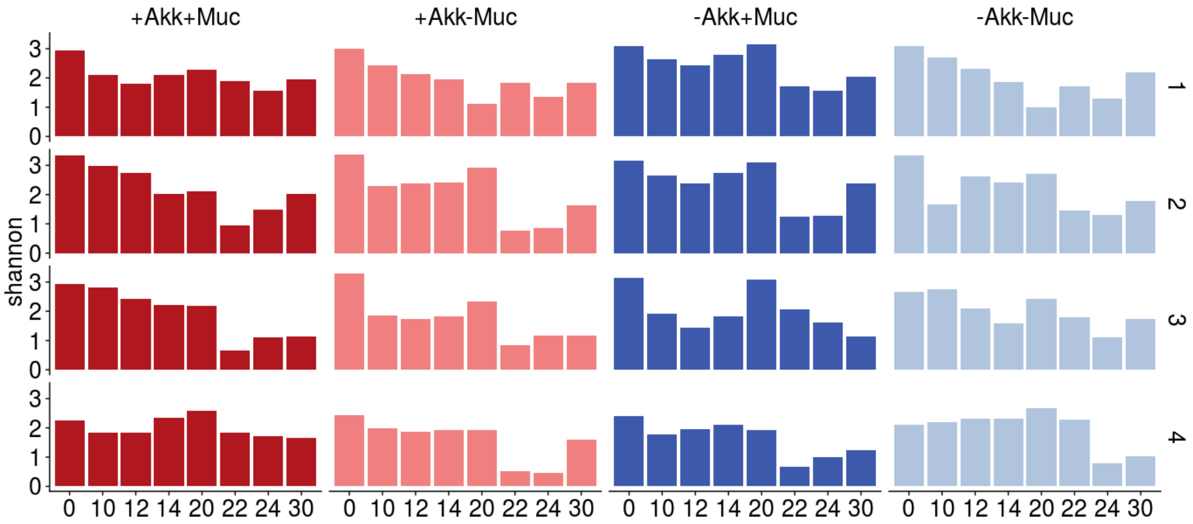


Supplementary Figure 3:qPCR analysis of 16S rRNA gene showing the response of the total acterial counts to the antibiotic pulse for the different donors and treatments.

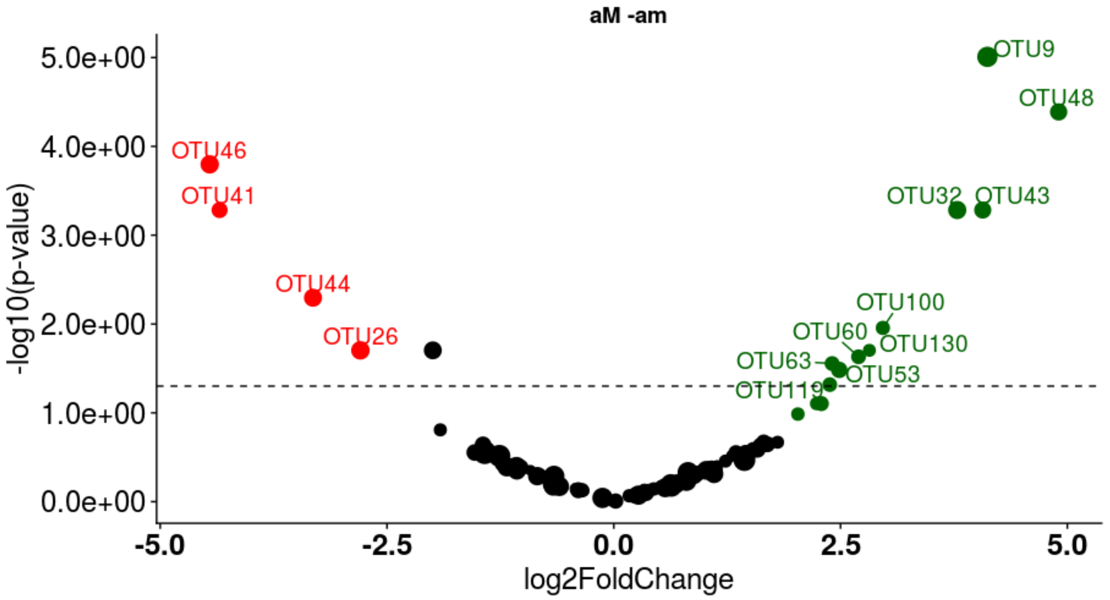


Supplementary Figure 4: Volcano plot showing results from the DESeq2 analysis showing the significantly (p<0.01) affected genera by antibiotic disturbance for each treatment (AM=+Akk+Muc; aM=-Akk+Muc;

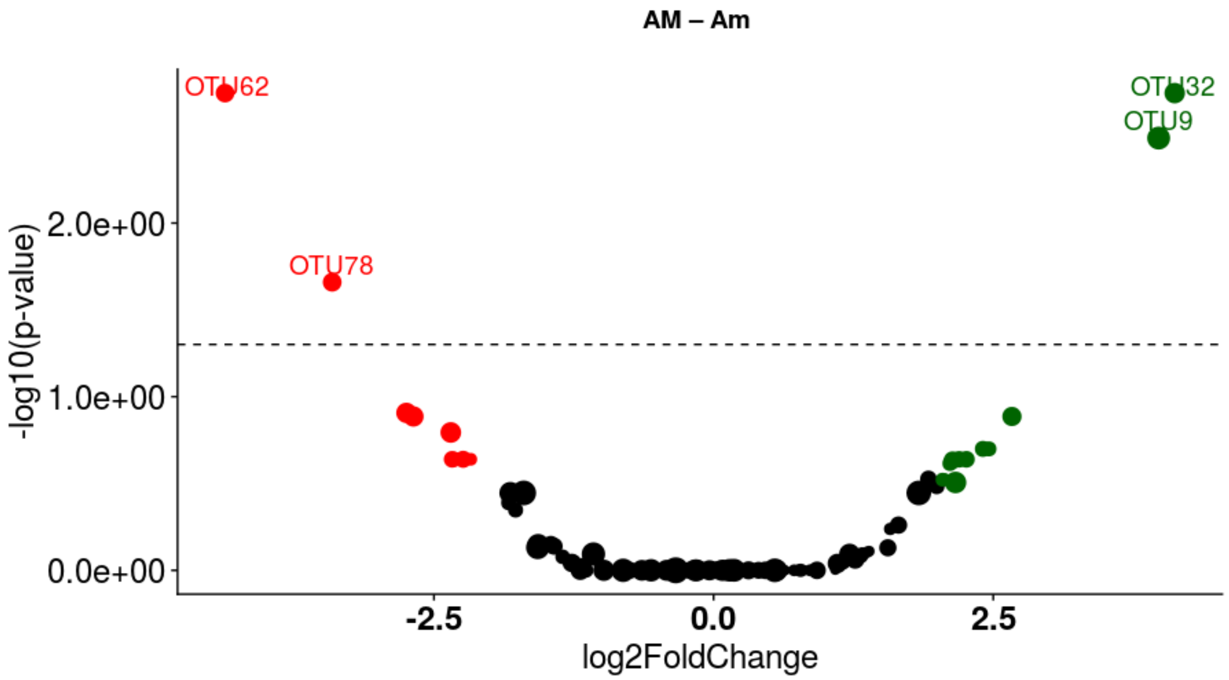
Am=+Akk-Muc; am=-Akk-Muc). Green and red dots show OTUs more abundant before and after antibiotic disturbance, respectively, and the size indicates the relative abundance of the OTU in the community.



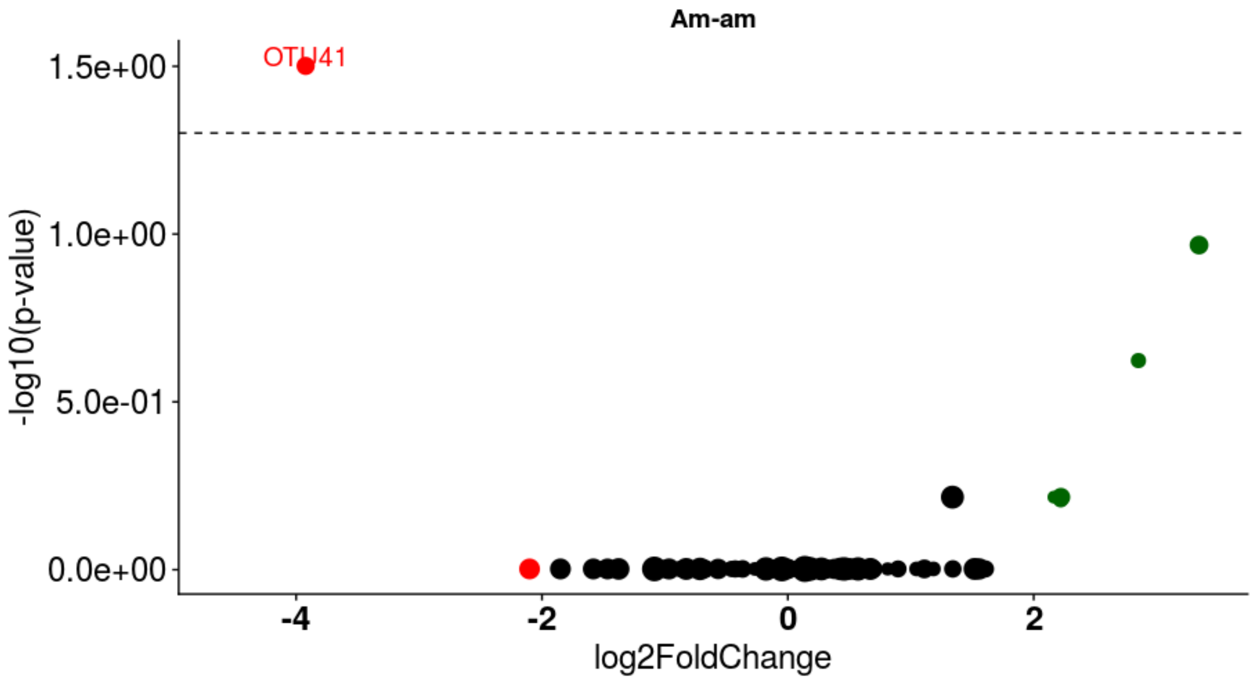
Supplementary Figure 5: Alpha-diversity, measured by Shannon coefficient, over time (Days) for the different donors and treatments.



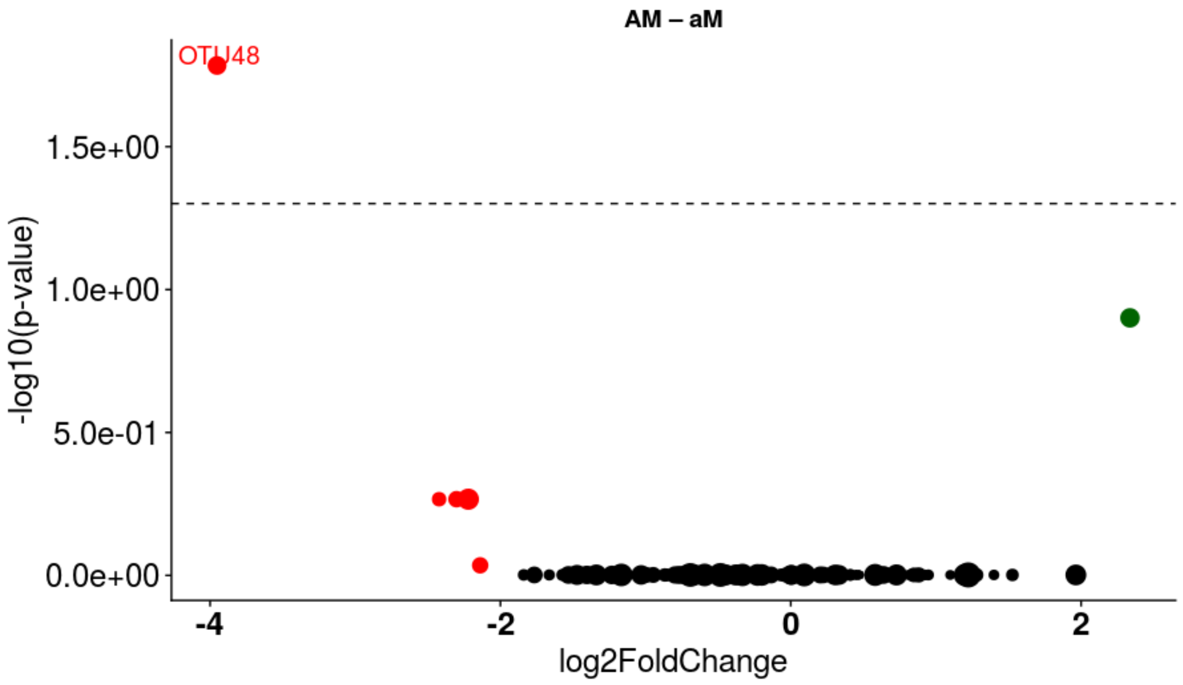
Supplementary Figure 6: Volcano plot showing results from the DESeq2 analysis comparing treatments " –Akk+Muc" and "-Akk-Muc". Green and red dots show OTUs more abundant in "-Akk+Muc", respectively, "- Akk- Muc" and the size indicates the relative abundance of the OTU in the community.



Supplementary Figure 7: Volcano plot showing results from DESeq2 analysis between treatments “ + Akk+Muc” and “+Akk-Muc”. Green dot show OTUs more abundant in “+Akk+Muc”, red dots for “+ Akk- Muc” and the size indicates relative abundance of the OTU in the community.



Supplementary Figure 8: Volcano plot showing results from DESeq2 analysis between treatments “ + Akk-Muc” and “-Akk-Muc”. Green dot show OTUs more abundant in “+Akk-Muc”, red dots for “- Akk- Muc” and the size indicates relative abundance of the OTU in the community.



Supplementary Figure 9: Volcano plot showing results from DESeq2 analysis between treatments " + Akk+Muc" and "-Akk+Muc". Green dot show OTUs more abundant in "+Akk+Muc", red dots for "- Akk+ Muc" and the size indicates relative abundance of the OTU in the community.

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